

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/718,952 A  
Source: 1Fw16  
Date Processed by STIC: 1/19/06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 01/19/2006

PATENT APPLICATION: US/10/718,952A

TIME: 12:52:09

Input Set : A:\BB1077 US DIV SUBSTITUTE SEQUENCE LISTING.txt

Output Set: N:\CRF4\01192006\J718952A.raw

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3 <110> APPLICANT: Hitz, William
4     Sebastian, Scott
5     Grace, John
6     Streit, Leon
8 <120> TITLE OF INVENTION: SOYBEAN PLANT PRODUCING SEEDS WITH REDUCED LEVELS OF
RAFFINOSE
9     SACCHARIDES AND PHYTIC ACID
11 <130> FILE REFERENCE: BB1077 US DIV
13 <140> CURRENT APPLICATION NUMBER: 10/718,952A
14 <141> CURRENT FILING DATE: 2003-11-21
16 <150> PRIOR APPLICATION NUMBER: 10/025,003
17 <151> PRIOR FILING DATE: 2002-03-11
19 <150> PRIOR APPLICATION NUMBER: 09/299,315
20 <151> PRIOR FILING DATE: 1999-04-26
22 <150> PRIOR APPLICATION NUMBER: PCT/US98/06822
23 <151> PRIOR FILING DATE: 1998-04-07
25 <150> PRIOR APPLICATION NUMBER: 08/835,751
26 <151> PRIOR FILING DATE: 1997-04-08
28 <160> NUMBER OF SEQ ID NOS: 20
30 <170> SOFTWARE: Microsoft Office 97
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1760
34 <212> TYPE: DNA
35 <213> ORGANISM: Glycine max
37 <400> SEQUENCE: 1
38 ctcttcttta ttcttttgt aatttcattc attcttaatc tttgtgaaaa ataatgttca    60
39 tgcagaattt taaggttgag tgtcctaata tgaagtacac cgagactgag attcagtcgc    120
40 tctacaacta cgaaaccacc gaacttggtc acgagaacag gaatggcacc tatcagtgga    180
41 ttgtcaaacc caaatctgtc aaatacgaat ttaaaaccaa catccatggt cctaaattag    240
42 gggtaatgct tgtgggttgg ggtggaaaca acggctcaac cctcacgggt ggtgttattg    300
43 ctaaccgaga gggcatttca tgggctacaa aggacaagat tcaacaagcc aattactttg    360
44 gctccctcac ccaagcctca gctatccgag ttgggtcctt ccaggagag gaaatctatg    420
45 cccattcaa gagcctgctt ccaatggtta accctgaaga catttgtgtt gggggatggg    480
46 atatcagcaa catgaacctg gctgatgcca tggccagggc aaaggtgttt gacatcgatt    540
47 tgcagaagca gttgaggcct tacatggaat ccatgcttcc actccccgga atctatgacc    600
48 cggatttcat tgetgccaac caagaggagc gtgccaacaa cgtcatcaag ggcacaaagc    660
49 aagagcaagt tcaacaatc atcaaagaca tcaaggcggt taaggaagcc accaaagtgg    720
50 acaaggtggt tgtactgtgg actgccaaca cagagaggta cagtaatttg gttgtgggcc    780
51 ttaatgacac catggagaat ctcttggttg ctgtggacag aaatgaggct gagatttctc    840
52 ctccacctt gtatgccatt gcttgtgtta tggaaaatgt tcctttcatt aatggaagcc    900
53 ctcaaacac ttttgtacca gggctgattg atcttgccat cgcgaggaac actttgattg    960
54 gtggagatga cttcaagagt ggtcagacca aaatgaaatc tgtgttggtt gatttccttg    1020
55 tgggggctgg tatcaagcca acatctatag tcagttacaa ccatctggga aacaatgatg    1080
56 gtatgaatct ttcggctcca caaactttcc gttccaagga aatctccaag agcaacgttg    1140

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57 ttgatgatat ggtcaacagc aatgccatcc tctatgagcc tgggtgaacat ccagaccatg 1200
58 ttgttggttat taagtatgtg ccttacgtag gggacagcaa gagagccatg gatgagtaca 1260
59 cttcagagat attcatgggt ggaaagagca ccattgtttt gcacaacaca tgcgaggatt 1320
60 cctcttagc tgcctctatt atcttggact tggctccttct tgcctgagctc agcactagaa 1380
61 tcgagtttaa agctgaaaat gagggaaaat tccactcatt ccaccagtt gctaccatcc 1440
62 tcagctacct caccaaggct cctctggttc caccgggtac accagtgggtg aatgcattgt 1500
63 caaagcagcg tgcaatgctg gaaaacataa tgagggtctg tgttggttg gccccagaga 1560
64 ataacatgat tctcgagtac aagtgaagca tgggaccgaa gaataatata gttggggtag 1620
65 cctagctgaa tgttttatgt taataatatg tttgcttata attttgcaag tgtaattgaa 1680
66 tgcacagct tcattaatgc tttagagcgg ggcataattct gtttactagg aacatgaatg 1740
67 aatgtagtat aattttgtgt                                     1760
69 <210> SEQ ID NO: 2
70 <211> LENGTH: 510
71 <212> TYPE: PRT
72 <213> ORGANISM: Glycine max
74 <400> SEQUENCE: 2
75 Met Phe Ile Glu Asn Phe Lys Val Glu Cys Pro Asn Val Lys Tyr Thr
76   1           5           10           15
78 Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
79           20           25           30
81 His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
82           35           40           45
84 Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
85           50           55           60
87 Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
88   65           70           75           80
90 Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
91           85           90           95
93 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
94           100          105          110
96 Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
97           115          120          125
99 Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
100          130          135          140
102 Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
103 145          150          155          160
105 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
106          165          170          175
108 Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
109          180          185          190
111 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
112          195          200          205
114 Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
115          210          215          220
117 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
118 225          230          235          240
120 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
121          245          250          255
123 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val

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124          260          265          270
126 Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
127          275          280          285
129 Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
130          290          295          300
132 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
133 305          310          315          320
135 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
136          325          330          335
138 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
139          340          345          350
141 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
142          355          360          365
144 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
145          370          375          380
147 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
148 385          390          395          400
150 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
151          405          410          415
153 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
154          420          425          430
156 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
157          435          440          445
159 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
160          450          455          460
162 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
163 465          470          475          480
165 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
166          485          490          495
168 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
169          500          505          510
171 <210> SEQ ID NO: 3
172 <211> LENGTH: 35
173 <212> TYPE: DNA
174 <213> ORGANISM: Artificial Sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
oligonucleotide
179 <400> SEQUENCE: 3
180 gggaattcca tatgttcacg gagaatttta aggtt
182 <210> SEQ ID NO: 4
183 <211> LENGTH: 39
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic oligonucleotide
190 <400> SEQUENCE: 4
191 aaggaaaaaa gcggccgctc acttgctacg gagaatcat
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 1533

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195 &lt;212&gt; TYPE: DNA

196 &lt;213&gt; ORGANISM: Glycine max

198 &lt;400&gt; SEQUENCE: 5

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199 atgttcacg agaatttttaa ggttgagtgt cctaattgtga agtacaccga gactgagatt 60
200 cagtccgtgt acaactacga aaccaccgaa cttgttcacg agaacaggaa tggcacctat 120
201 cagtggattg tcaaacccaa atctgtcaaa tacgaattta aaaccaacat ccatgttccct 180
202 aaattagggg taatgcttgt gggttggggg ggaacaacg gctcaaccct caccggtggg 240
203 gttattgcta accgagaggg catttcatgg gctacaaagg acaagattca acaagccaat 300
204 tactttggct ccctcaccca agcctcagct atccgagttg ggtccttcca gggagaggaa 360
205 atctatgccc cattcaagag cctgcttcca atgggttaacc ctgacgacat tgtgtttggg 420
206 ggatgggata tcagcaacat gaacctggct gatgccatgg ccagggcaaa ggtgtttgac 480
207 atcgatttgc agaagcagtt gaggccttac atggaatcca tgcttccact ccccggaatc 540
208 tatgacccgg atttcattgc tgccaaccaaa gaggagcgtg ccaacaacgt catcaagggc 600
209 acaaagcaag agcaagttca acaaatcatc aaagacatca aggcgtttta ggaagccacc 660
210 aaagtggaca aggtggttgt actgtggact gccaacacag agaggtacag taatttggtt 720
211 gtgggcctta atgacaccat ggagaatctc ttggctgctg tggacagaaa tgaggctgag 780
212 atttctcctt ccaccttgta tgccattgct tgtgttatgg aaaatgttcc ttccattaat 840
213 ggaagccctc agaacacttt tgtaccaggg ctgattgata ttgccatcgc gaggaacact 900
214 ttgattgggtg gagatgactt caagagtggg cagaccaaaa tgaaatctgt gttggttgat 960
215 ttccttgtgg gggctgggat caagccaaca tctatagtca gttacaacca tctgggaaac 1020
216 aatgatggta tgaatctttc ggctccacaa actttccgtt ccaaggaaat ctccaagagc 1080
217 aacgttggtg atgatatggg caacagcaat gccatcctct atgagcctgg tgaacatcca 1140
218 gaccatgttg ttgttattaa gtatgtgcct tacgtagggg acagcaatag agccatggat 1200
219 gagtacactt cagagatatt catgggtgga aagagcacca ttgttttgca caacacatgc 1260
220 gaggattccc tcttagctgc tctattatc ttggacttgg tcttcttgc tgagctcagc 1320
221 actagaatcg agtttaaagc tgaaaatgag ggaaaattcc actcattcca ccagttgct 1380
222 accatcctca gctacctcac caaggctcct ctgggtccac cgggtacacc agtggatgaat 1440
223 gcattgtcaa agcagcgtgc aatgctggaa aacataatga gggcttgtgt tggattggcc 1500
224 ccagagaata acatgattct cgagtacaag tga 1533

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226 &lt;210&gt; SEQ ID NO: 6

227 &lt;211&gt; LENGTH: 510

228 &lt;212&gt; TYPE: PRT

229 &lt;213&gt; ORGANISM: Glycine max

231 &lt;400&gt; SEQUENCE: 6

```

232 Met Phe Ile Glu Asn Phe Lys Val Glu Cys Pro Asn Val Lys Tyr Thr
233   1           5           10           15
235 Glu Thr Glu Ile Gln Ser Val Tyr Asn Tyr Glu Thr Thr Glu Leu Val
236           20           25           30
238 His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
239           35           40           45
241 Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
242           50           55           60
244 Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
245 65           70           75           80
247 Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
248           85           90           95
250 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
251           100          105          110
253 Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu

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254          115          120          125
256 Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
257          130          135          140
259 Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
260 145          150          155          160
262 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
263          165          170          175
265 Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
266          180          185          190
268 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
269          195          200          205
271 Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
272          210          215          220
274 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
275 225          230          235          240
277 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
278          245          250          255
280 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
281          260          265          270
283 Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
284          275          280          285
286 Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
287          290          295          300
289 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
290 305          310          315          320
292 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
293          325          330          335
295 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
296          340          345          350
298 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
299          355          360          365
301 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
302          370          375          380
304 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Asn Arg Ala Met Asp
305 385          390          395          400
307 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
308          405          410          415
310 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
311          420          425          430
313 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
314          435          440          445
316 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
317          450          455          460
319 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
320 465          470          475          480
322 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
323          485          490          495
325 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
326          500          505          510

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**VERIFICATION SUMMARY**

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